



Host Range Profile of *Stagonosporopsis citrulli* (IIHR-GSB27): The Muskmelon Gummy Stem Blight Pathogen

H.K. DHANUSHREE¹., G.M. SANDEEP KUMAR^{1*}., S. SRIRAM¹., RAO, E.S²., MANJUNATH GOWDA, D.C²., N.R. PRASANNAKUMAR¹ and GAURAV YASWANTH RAKHONDE¹.

¹Division of Crop Protection, ²Division of Vegetable Science ICAR-Indian Institute of Horticultural Research, Hesaraghatta lake post, Bengaluru-560089, India

*E-mail: sandeepmycologist@gmail.com

ABSTRACT: Gummy stem blight (GSB) is an emerging disease of muskmelon (*Cucumis melo* L.) in India. This study documents the experimental host range of *Stagonosporopsis citrulli* isolate IIHR-GSB27. Host range assessment was conducted through detached leaf inoculation on 23 cucurbit crops and collar inoculation on 19 cucurbit crops commonly cultivated in India. Muskmelon and watermelon consistently exhibited very high disease severity in both assays, confirming high aggressiveness of the isolate. Several crops, including summer squash, winter squash, oriental pickling melon, snap melon, long melon and sambar cucumber, showed moderate to high susceptibility. In contrast, pumpkin, bottle gourd and bitter gourd showed low to no disease development in both assays. Correlation analysis showed a strong and significant positive relationship between disease severities recorded in detached leaf and collar inoculation assays, indicating good agreement between the two methods. These findings underscore the epidemiological significance of collateral cucurbit hosts in pathogen survival and spread, highlighting the need to incorporate host range information into crop rotation, cropping sequence and integrated disease management strategies for sustainable control of gummy stem blight in muskmelon-based production systems in India.

Key words: Experimental host range, *Stagonosporopsis citrulli*, muskmelon, India

INTRODUCTION

Gummy stem blight (GSB) of cucurbits is caused by a species complex within the genus *Stagonosporopsis*, comprising *S. cucurbitacearum* (syn. *Didymella bryoniae*), *S. citrulli* and *S. caricae*, which are genetically distinct but morphologically similar (Aveskamp *et al.*, 2010; Brewer *et al.*, 2015; Stewart *et al.*, 2015). Members of the *Stagonosporopsis* species complex exhibit a wide host range, infecting 37 cucurbit species across 21 genera and three tribes (Rennberger and Keinath, 2018). All three species are pathogenic to cucurbits belonging to the genera *Cucumis*, *Citrullus* and *Cucurbita*, with watermelon and muskmelon generally reported as highly susceptible, while several *Cucurbita* species display partial resistance or lower disease severity (Keinath, 2014a; Stewart *et al.*, 2015). Such broad host adaptability facilitates cross-infectivity among cucurbit hosts, allowing the pathogen to persist on alternate hosts that may act as reservoirs of inoculum and contribute to disease carry-over in crop sequences and mixed cropping systems.

Strategies to manage plant disease from use of resistant varieties to crop rotation, elimination of reservoirs, landscape planning, surveillance, quarantine,

risk modelling and anticipation of disease emergences all rely on knowledge of pathogen host range (Morris and Moury, 2019). Despite the epidemiological significance of host range, experimental information on the host range of muskmelon-derived GSB pathogen under Indian scenario remains limited. In India, the disease was first reported in the country on chayote and bottle gourd at Hesaraghatta, IIHR, Bengaluru (Sohi and Om-Prakash, 1972) and subsequently on other cucurbit crops *viz.*, cucumber (Kumar and Khan, 1984), bitter gourd (Kulwant and Shetty, 1996), ash gourd (Pandey and Pandey, 2003), muskmelon (Sudisha *et al.*, 2004), gherkin (Garampalliet *al.*, 2016), ridge gourd (Bhat *et al.*, 2018), watermelon (Mahapatra *et al.*, 2020), ivy gourd (Savitha and Garampalli, 2022).

Most available reports are based on isolated host records rather than systematic cross-infectivity assessments across multiple cucurbit hosts. Understanding host susceptibility patterns is essential for predicting disease spread, identifying collateral hosts and designing effective crop rotation and integrated disease management strategies. Therefore, the present study was undertaken to document the experimental host range of gummy stem blight pathogen of muskmelon.

MATERIALS AND METHODS

Source of the pathogen

The gummy stem blight pathogen used in host range assessment was isolated from a muskmelon field in Tumakuru district of Karnataka, India (13°49'40.7"N, 76°46'31.3"E). The isolate obtained was designated IIHR-GSB27 and identified based on morphological, pathogenic and molecular characteristics. Cultural features were recorded on quarter-strength PDA and colony morphology and pigmentation were assessed using standard taxonomic descriptions for *Stagonosporopsis* spp. Molecular identification was performed using species-specific microsatellite markers and multilocus sequencing of the *ITS*, *LSU* and *β-tubulin* (*TUB*) regions. Based on combined morphological and molecular evidence, isolate IIHR-GSB27 was identified as *Stagonosporopsis citrulli*. GenBank accession numbers of the isolate are PX242833 for *ITS*, PX242933 for *LSU* and PX257361 for *TUB*. The isolate was found pathogenic on leaves and collar of muskmelon (*Cucumis melo* L.) cv. Arka Siri at the two-true leaf stage with mycelial plugs inoculation (Dhanushree *et al.*, 2025).

Plant Material

The host range of the muskmelon GSB isolate IIHR-GSB27 was assessed using detached leaf and collar inoculation assays. Detached leaf assays were conducted on 23 cucurbitaceous crops, while collar inoculation assays were performed on 19 cucurbitaceous crops, representing diverse genera within the Cucurbitaceae (Table 1). Healthy seedlings were raised in sterilized cocopeat under glasshouse conditions, muskmelon cv. Arka Siri served as the susceptible control.

Host range documentation-Detached leaf assay

For the detached leaf assay, fully expanded and healthy leaves were collected from 30-day-old seedlings and placed on inverted, autoclaved 90-mm Petri plates within a plastic container. The adaxial leaf surface was

gently pin-pricked and an 8-mm mycelial disc excised from the actively growing margin of a 7-day-old culture of isolate IIHR-GSB27 was positioned on the wound with the mycelial side facing the leaf surface. High humidity was maintained and leaf desiccation was prevented by attaching a sterile water-soaked cotton swab to the petiole, with additional moistened swabs placed at the corners of the container (Zhao *et al.*, 2018; Jeong *et al.*, 2022). The experiment was conducted in a completely randomized design (CRD) with three replications, each consisting of three leaves. Disease severity was quantified using an image-based approach across 23 cucurbit crops. Three inoculated leaves from each replication were scanned and digital images were analysed using ImageJ software to determine the percentage of diseased leaf area at 15 days after incubation (Pride *et al.*, 2020; Lavanya *et al.*, 2023).

Host range documentation-Collar inoculation assay

Collar inoculation was carried out on 14-day-old seedlings by placing 8-mm mycelial discs, obtained from hyphal tips of actively growing 7-day-old cultures of the muskmelon GSB isolate IIHR-GSB27, at the collar region with the mycelial surface in direct contact with plant tissue. The inoculum was secured using cellophane tape. The experiment was conducted in a completely randomized design (CRD) with three replications, each replication comprising three plants. Inoculated muskmelon cv. Arka Siri seedlings were maintained as controls (Sudisha *et al.*, 2004; Nuangmeket *et al.*, 2018). Disease assessment was performed when seedlings exhibited complete wilting and the per cent disease index (PDI) was determined using a 0–4 disease rating scale for stem infection as described by Zhang *et al.* (2017). Disease severity was classified based on the proportion of stem area affected: 0 = no symptoms, 1 = 0–25%, 2 = 25–50%, 3 = 50–75% and 4 = >75%. The PDI was calculated using the formula proposed by McKinney (1923).

$$\text{PDI} = \frac{\text{Sum of all numerical disease ratings}}{\text{Total number of observations} \times \text{Maximum disease grade}} \times 100$$

Table 1. List of cucurbitaceous crops tested as host for the muskmelon GSB isolate IIHR-GSB27

Sl. No.	Common Name	Scientific Name	Genotype	Assay
1	Ash gourd	<i>Benincasa hispida</i> (Thunb.) Cogn.	Big Round	Collar and leaf
2	Bitter gourd	<i>Momordica charanita</i> L.	Green Long	Collar and leaf
3	Bottle gourd	<i>Lagenaria siceraria</i> (Molina) Standl.	BG24	Collar and leaf
4	Chayote	<i>Sechium edule</i> (Jacq.) Sw.	Local	Leaf

5	Slicing cucumber	<i>Cucumis sativus</i> (L.)	Arka Veera	Collar and leaf
6	Gherkin (Pickling cucumber)	<i>Cucumis sativus</i> (L.)	Keerthi	Collar and leaf
7	Ivy gourd	<i>Coccinia grandis</i> (L.) Voigt	Arka Neelachal Kunkhi	Leaf
8	Long melon	<i>Cucumis melo</i> var. <i>utilissimus</i> (Roxb.) Duth. & Full.	A252	Collar and leaf
9	Muskmelon	<i>Cucumis melo</i> (L.)	Arka Siri	Collar and leaf
10	Oriental pickling melon	<i>Cucumis melo</i> var. <i>Conomon</i> (Thunb.) Makino	A391	Collar and leaf
11	Pointed gourd (Parwal)	<i>Trichosanthes dioica</i> Roxb.	Swarna Rekha	Leaf
12	Pumpkin	<i>Cucurbita moschata</i> Duchesne	Arka Suryamukhi	Collar and leaf
13	Ridge gourd	<i>Luffa acutangula</i> (L.) Roxb	Arka Prasan	Collar and leaf
14	Round melon	<i>Praecitrullus fistulosus</i> (Stocks) Pangalo	Arka Tinda	Collar and leaf
15	Sambar cucumber	<i>Cucumis sativus</i> L.var. <i>sativus</i>	Sambar	Collar and leaf
16	Snake gourd	<i>Trichosanthes cucumerina</i> L.	9098	Collar and leaf
17	Snap melon	<i>Cucumis melo</i> var. <i>momordica</i> (Roxb.) Duthie & J. B. Fuller	A253	Collar and leaf
18	Sponge gourd	<i>Luffa aegyptiaca</i> Mill.	Local	Collar and leaf
19	Summer squash	<i>Cucurbita pepo</i> L.	Australian Green	Collar and leaf
20	Summer squash	<i>Cucurbita pepo</i> L.	Pusa Alankar	Collar and leaf
21	Teasel gourd	<i>Momordica dioica</i> Roxb.	Arka Bharath	Leaf
22	Watermelon	<i>Citrullus lanatus</i> (Thunb.) Matsum. & Nakai	Arka Muthu	Collar and leaf
23	Winter squash	<i>Cucurbita maxima</i> Duchesne	Arka Chandan	Collar and leaf

Statistical analysis

Experimental data were analyzed by analysis of variance (ANOVA) using R Studio software (version 2024.12.1+563). Percentage values were arcsine transformed prior to analysis and treatment means were separated using Duncan's Multiple Range Test at the 1% level of significance. Correlation analysis and scatter plots were performed using the same software.

RESULTS AND DISCUSSION

Host range - Detached leaf assay

The detached leaf assay performed on 23 cucurbitaceous crops demonstrated that the muskmelon GSB isolate IIHR-GSB27 has a wide host range within

the Cucurbitaceae, with distinct differences in host susceptibility as indicated by the per cent leaf disease area (Table 2; Fig. 1). Muskmelon (Arka Siri), the original host, exhibited severe disease development (95.14% leaf disease area), confirming the high aggressiveness of the isolate, while watermelon (Arka Muthu) recorded the highest disease severity (96.41%), indicating strong cross-infectivity between *Cucumis* and *Citrullus* hosts. High to moderate disease levels were also observed on summer squash (Pusa Alankar and Australian Green), winter squash, oriental pickling melon, round melon, long melon and snake gourd (51.08–93.62%), suggesting a high degree of host compatibility and limited host specificity within these cucurbits. In contrast, pumpkin, bottle gourd, bitter gourd, slicing and

pickling cucumbers, ash gourd, ivy gourd and pointed gourd showed consistently low disease severity (<20%), indicating reduced susceptibility or partial resistance to the isolate. Several crops, including ridge gourd, snap melon, sambar cucumber, chayote, sponge gourd and teasel gourd, exhibited intermediate disease responses, reflecting quantitative variation in host reaction. Overall, the data highlight a clear gradient in disease severity across the tested cucurbit hosts, reflecting distinct susceptibility levels and confirming the broad host range of isolate IIHR-GSB27 with variable aggressiveness.

Host range - Collar inoculation assay

Collar inoculation using the muskmelon GSB isolate IIHR-GSB27 revealed a broad host range among 19 cucurbitaceous crops evaluated, with marked differences in disease severity as reflected by the percent disease index assessed at 3 days post-inoculation (Table 3; Fig. 2). Muskmelon, watermelon, summer squash (Australian Green) and oriental pickling melon exhibited complete susceptibility, each recording 100 % disease index

(PDI), indicating a high degree of host compatibility and aggressive colonization by the isolate. High disease severity was also noted in summer squash (Pusa Alankar) and sambar cucumber, which exhibited PDI values of 91.67 and 83.33 per cent, respectively, suggesting strong but comparatively reduced susceptibility. Moderate levels of infection were recorded in snap melon and ash gourd (58.33%), followed by round melon and long melon (41.67%), winter squash, snake gourd and sponge gourd (33.33%), and pickling and slicing cucumbers, which showed lower but detectable disease development. In contrast, pumpkin and bottle gourd exhibited minimal disease expression (8.33%), while ridge gourd and bitter gourd remained completely symptomless, indicating a high level of resistance or non-host response to the isolate. These results demonstrate marked variation in host susceptibility within the Cucurbitaceae, with the IIHR-GSB27 isolate displaying pronounced pathogenicity on several economically important cucurbits, while others exhibited partial to complete resistance under collar inoculation conditions.

Table 2. Host range documentation by detached leaf assay of the muskmelon GSB isolate IIHR-GSB27 on 23 cucurbitaceous crops

Sl. No.	Cucurbitaceous crop	Per cent leaf disease area (%)
1	Muskmelon (Arka Siri)	95.14 ^{ab} (77.27)*
2	Watermelon (Arka Muthu)	96.41 ^a (79.09)
3	Pumpkin (Arka Suryamukhi)	3.53 ^q (10.82)
4	Winter squash (Arka Chandan)	76.20 ^d (60.79)
5	Summer squash (Australian Green)	93.42 ^c (75.12)
6	Summer squash (Pusa Alankar)	93.62 ^{bc} (75.37)
7	Bottle gourd (BG24)	5.37 ^p (13.38)
8	Round melon (Arka Tinda)	63.37 ^f (52.74)
9	Ridge gourd (Arka Prasan)	17.95 ⁱ (25.05)
10	Pickling Cucumber-Gherkin (Keerthi)	9.01 ^o (17.46)
11	Slicing cucumber (Arka Veera)	4.42 ^{pq} (12.11)
12	Snap melon (A253)	48.57 ^r (44.16)
13	Long melon (A252)	60.13 ^g (50.82)
14	Oriental pickling melon (A391)	71.60 ^e (57.78)
15	Bitter gourd (Green Long)	5.70 ^p (13.79)

16	Ash gourd (Big Round)	11.41 ⁿ (19.73)
17	Snake gourd (9098)	51.08 ^h (45.60)
18	Sambar cucumber (Sambar)	34.63 ^j (36.03)
19	Ivy gourd (Arka Neelachal Kunkhi)	14.03 ^m (21.97)
20	Chayote (Local)	22.40 ^k (28.23)
21	Sponge gourd (Local)	35.35 ^j (36.46)
22	Teasel gourd (Arka Bharath)	22.50 ^k (28.30)
23	Pointed gourd (Swarna Rekha)	15.20 ^m (22.93)
C.D @1%		1.32
SE(m)±		0.46
C.V.		2.04

*Values in parentheses are arc-sine transformed

Table 3. Host range documentation by collar inoculation of 19 cucurbitaceous crops with the muskmelon GSB isolate IIHR-GSB27

Sl. No.	Cucurbitaceous host	Per cent disease index (%)
1	Muskmelon (Arka Siri)	100.00 ^a (89.96)
2	Watermelon (Arka Muthu)	100.00 ^a (89.96)
3	Pumpkin (Arka Suryamukhi)	8.33 ⁱ (16.77)
4	Winter squash (Arka Chandan)	33.33 ^f (35.25)
5	Summer squash (Australian Green)	100.00 ^a (89.96)
6	Summer squash (Pusa Alankar)	91.67 ^b (73.42)
7	Bottle gourd (BG24)	8.33 ⁱ (16.77)
8	Round melon (Arka Tinda)	41.67 ^e (40.18)
9	Ridge gourd (Arka Prasan)	0.00 ^j (0.00)
10	Pickling Cucumber-Gherkin (Keerthi)	25.00 ^g (29.99)
11	Slicing cucumber (Arka Veera)	16.67 ^h (24.08)
12	Snap melon (A253)	58.33 ^d (49.78)
13	Long melon (A252)	41.67 ^e (40.19)
14	Oriental pickling melon (A391)	100.00 ^a (89.96)
15	Bitter gourd (Green Long)	0.00 ^j (0.00)
16	Ash gourd (Big Round)	58.33 ^d (49.78)
17	Snake gourd (9098)	33.33 ^f (35.25)

18	Sambar cucumber (Sambar)	83.33 ^c (65.89)
19	Sponge gourd (Local)	33.33 ^f (35.25)
C.D @1%		1.62
SE(m)±		0.56
C.V.		2.13

*Values in parentheses are arc-sine transformed

Integrated host range assessment using the detached leaf assay and collar inoculation assay consistently demonstrate that the muskmelon GSB isolate IIHR-GSB27 possesses a broad host range within the Cucurbitaceae, with pronounced quantitative variation in host susceptibility. Both assays identified muskmelon and watermelon as highly susceptible hosts, confirming strong aggressiveness of the isolate and clear cross-infectivity between *Cucumis* and *Citrullus* species. Several cucurbits, including summer squashes, oriental pickling melon, snap melon and sambar cucumber, supported moderate to high levels of infection, indicating limited host specificity and a capacity of the isolate to infect multiple cultivated cucurbits. In contrast, pumpkin, bottle gourd and bitter gourd consistently expressed minimal to no disease across assays, reflecting stable resistance or a non-host response. The overall concordance between leaf-based and whole-plant collar inoculation responses highlights a clear gradient of susceptibility among cucurbit hosts and confirms that IIHR-GSB27 is a highly adaptable pathogen with variable aggressiveness depending on host species.

Correlation analysis

The correlation analysis and scatter plot demonstrate a strong and statistically significant

positive relationship between disease severity recorded by collar inoculation and the detached leaf assay across the 19 cucurbitaceous crops challenged with the muskmelon GSB isolate IIHR-GSB27 (Fig. 3). The Pearson correlation coefficient ($r = 0.802$; $P < 0.01$) indicates that crops exhibiting higher per cent leaf disease area in the detached leaf assay generally also developed higher per cent disease index following collar inoculation. This association is further supported by the linear regression ($y = 10.29 + 0.84x$), with an R^2 value of 0.644, suggesting that approximately 64 per cent of the variation in collar inoculation disease severity can be explained by responses observed in the detached leaf assay. The dispersion of points around the regression line reflects some host-specific deviation, likely due to differences in tissue susceptibility, infection courts and systemic spread between detached leaves and collar tissues. The overall trend confirms good concordance between the two pathogenicity assays, validating the detached leaf assay as a reliable and rapid proxy for assessing host response to GSB, while also emphasizing that collar inoculation captures additional aspects of disease development relevant under whole-plant conditions.

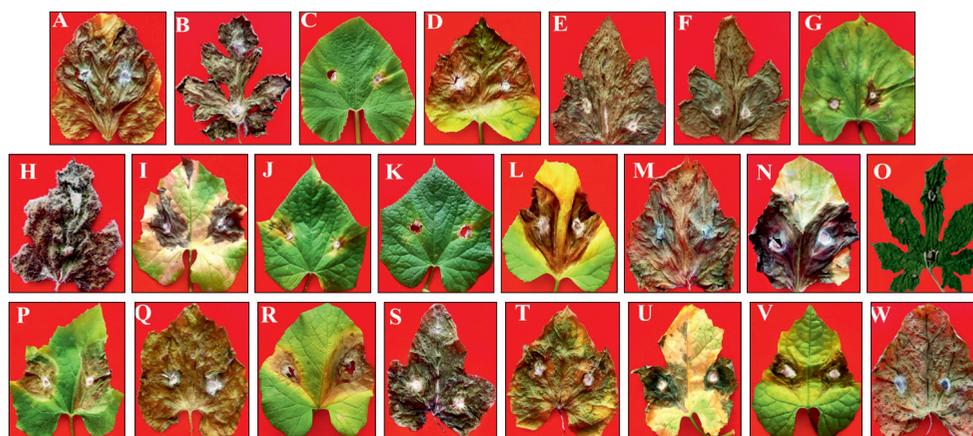


Fig. 1. Host range documentation by detached leaf assay of muskmelon GSB isolate IIHR-GSB27 on cucurbitaceous crops at 15 dpi. (A) Muskmelon; (B) Watermelon; (C) Pumpkin; (D) Winter Squash; (E) Summer Squash (Australian Green); (F) Summer Squash (Pusa Alankar); (G) Bottle gourd; (H) Round melon; (I) Ridge gourd; (J) Gherkin; (K) Cucumber; (L) Snap melon; (M) Long melon; (N) Oriental Pickling Melon; (O) Bitter gourd; (P) Ash gourd; (Q) Snake gourd; (R) Sambar Cucumber; (S) Ivy gourd; (T) Chayote; (U) Sponge gourd; (V) Teasel gourd; (W) Pointed gourd.

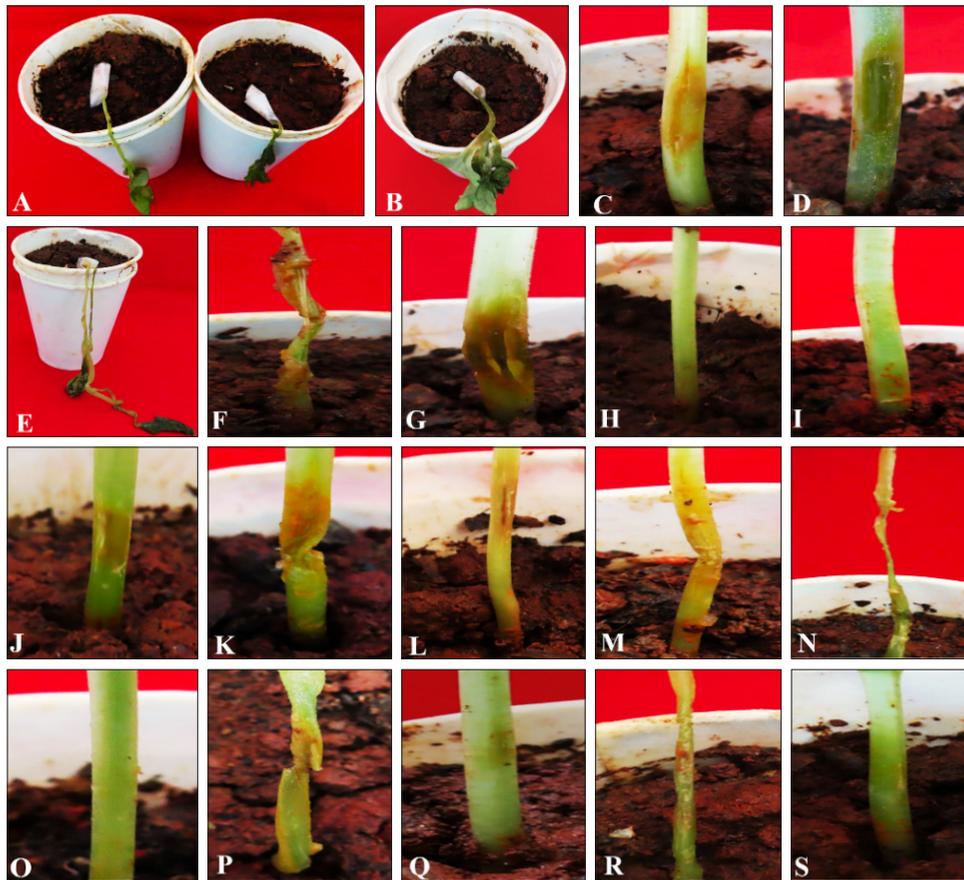


Fig. 2. Host range documentation by collar inoculation of 19 cucurbitaceous crops with muskmelon GSB isolate IHHR-GSB27. (A) Muskmelon; (B) Watermelon; (C) Pumpkin; (D) Winter Squash; (E) Summer Squash (Australian Green); (F) Summer Squash (Pusa Alankar); (G) Bottle gourd; (H) Roundmelon; (I) Ridge gourd; (J) Gherkin; (K) Cucumber; (L) Snap melon; (M) Long melon; (N) Oriental Pickling Melon; (O) Bitter gourd; (P) Ash gourd; (Q) Snake gourd; (R) Sambar Cucumber; (S) Sponge gourd.

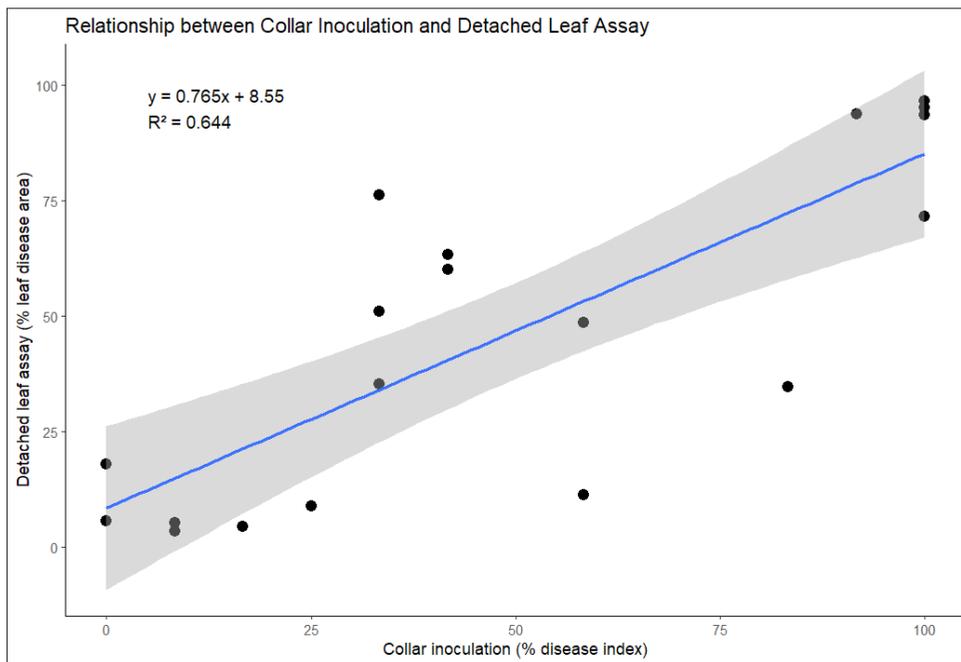


Fig. 3. Scatter plot showing the positive linear correlation existing between detached leaf assay (% leaf disease area) and collar inoculation assay (% disease index). Grey shade represents confidence interval.

The present investigation provides a robust and integrative assessment of the host range and relative aggressiveness of the muskmelon GSB isolate IIHR-GSB27, employing both detached leaf and collar inoculation assays across a wide spectrum of cucurbitaceous hosts. The combined use of these complementary pathogenicity assays strengthens the biological relevance of the findings by capturing both localized foliar susceptibility and whole-plant stem infection dynamics. The results demonstrate that IIHR-GSB27 is a highly adaptable pathogen with a broad host range within the Cucurbitaceae, exhibiting pronounced quantitative variation in disease expression rather than strict host specificity.

In India, several cucurbit crops have been documented as natural field hosts of *Stagonosporopsis* spp. Early reports identified *Didymella bryoniae* infecting chayote at Hesaraghatta, Bengaluru (Sohi and Om-Prakash, 1972), followed by its occurrence on cucumber (Kumar and Khan, 1984), bitter melon (Kulwant and Shetty, 1996), ash gourd (Pandey and Pandey, 2003) and muskmelon (Sudisha *et al.*, 2004). Subsequent studies reported the association of *Stagonosporopsis citrulli* and *S. caricae* with gherkin (Garampalli *et al.*, 2016), *D. bryoniae* on ridge gourd (Bhat *et al.*, 2018), *S. cucurbitacearum* on watermelon (Mahapatra *et al.*, 2020) and ivy gourd (Savitha and Garampalli, 2022).

High susceptibility of muskmelon and watermelon to GSB has been consistently reported, indicating that these crops provide highly favorable infection niches for *Stagonosporopsis* spp. Seblani *et al.* (2023) have demonstrated that *S. citrulli*, *S. caricae* and *S. cucurbitacearum* were all pathogenic on multiple cucurbit cultivars, with *S. citrulli* exhibiting the greatest aggressiveness. Similarly, Santos *et al.* (2009) and Keinath (2011) have reported that *Cucumis melo* and *Citrullus lanatus* generally support higher disease severity and pathogen reproduction than Cucurbita species. Collectively, these findings indicate that Cucumis-Citrullus hosts are central to gummy stem blight epidemiology in cucurbit production systems.

Moderate to high levels of disease severity on several cultivated cucurbits have also been reported, supporting the concept of limited host specialization among gummy GSB pathogens. Rennberger and Keinath (2018) have demonstrated that *S. citrulli* can infect a wide range of cultivated and wild cucurbit species, with marked variation in disease severity but no clear host restriction.

Stewart *et al.* (2015) have further demonstrated that all three major *Stagonosporopsis* species are pathogenic to *Citrullus*, *Cucumis* and *Cucurbita*, reflecting their shared evolutionary adaptation to cucurbit hosts. These observations suggest that non-primary cucurbit hosts may function as reservoirs, contributing to pathogen persistence and cross-infection.

In contrast, reduced susceptibility of pumpkin, bottle gourd and bitter melon has been reported in several studies. Keinath (2014b) has demonstrated that although *Didymella bryoniae* is capable of infecting multiple cucurbit species, disease severity and pathogen reproduction were substantially lower on *Cucurbita* spp. and *Lagenaria siceraria* than on muskmelon and watermelon. Similarly, Santos *et al.* (2009) have reported relatively high levels of resistance in pumpkin and chayote across diverse pathogen isolates. Such responses suggest the involvement of host-mediated resistance mechanisms that restrict colonization and disease progression.

The concordance between foliar and stem-based disease assessments has been documented previously. Keinath (2011) and Gimode *et al.* (2019) have reported that detached leaf assays reliably reflect whole-plant susceptibility to GSB, although variability associated with tissue-specific infection processes has also been observed. Collar and stem infections have been shown to play a critical role in vine collapse, pathogen reproduction and epidemic persistence, as demonstrated by Rennberger *et al.* (2019), emphasizing the epidemiological relevance of whole-plant infection.

CONCLUSION

The combined assays provide robust evidence of the wide host spectrum and variable aggressiveness of the muskmelon GSB isolate, emphasizing the importance of host selection in disease-prone regions. The identification of both highly susceptible and resistant cucurbit hosts offers valuable insights for integrated GSB management, including the development of resistant cultivars, strategic crop rotation and the deployment of grafting systems. Gummy stem blight is an emerging disease of cucurbits in India. The information on experimental host range generated in this study will help in risk analysis of further range expansion of this pathogen in different cucurbit growing areas of the country. Crop sequence patterns should take in to account this host range information so as to reduce pathogen survival and perpetuation.

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AUTHOR'S CONTRIBUTION

HKD, GMS, SS- collection, processing, conceptualisation, methodology, analysis writing the original draft, imaging and editing; RES, MGDC, NRP and GYR – planning, analysis, and final draft correction.

CONFLICT OF INTEREST

Authors do not have conflicts of interest to express

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